



11091003721 11091003722

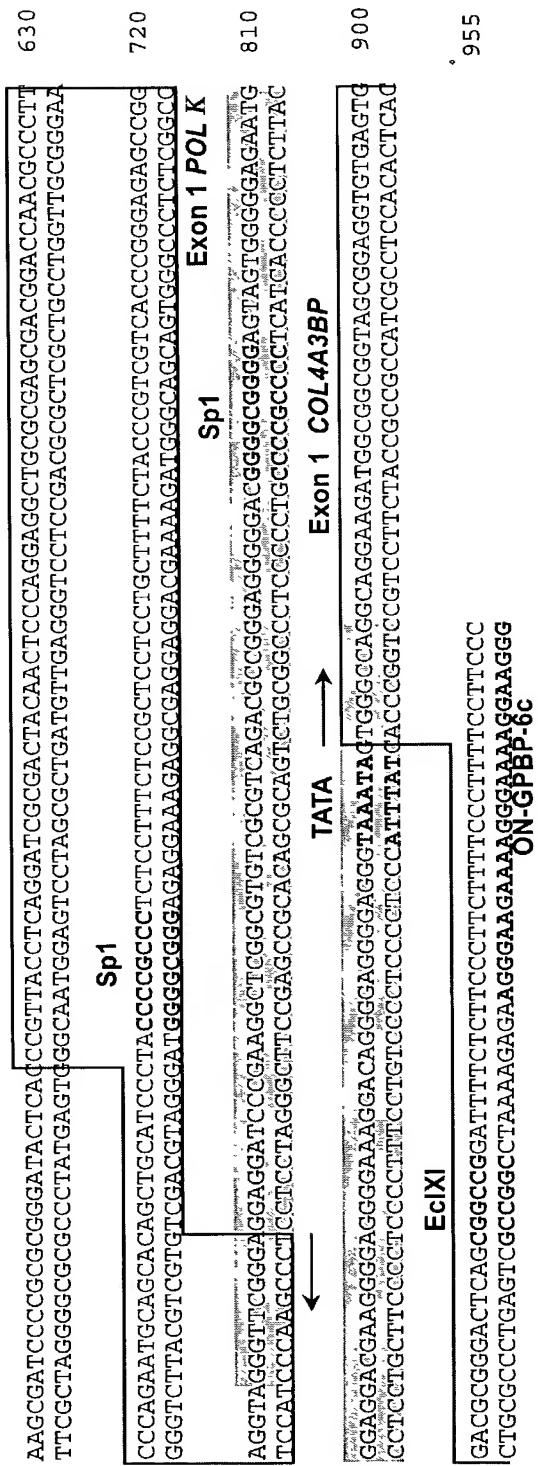
**FIGURE 1a**

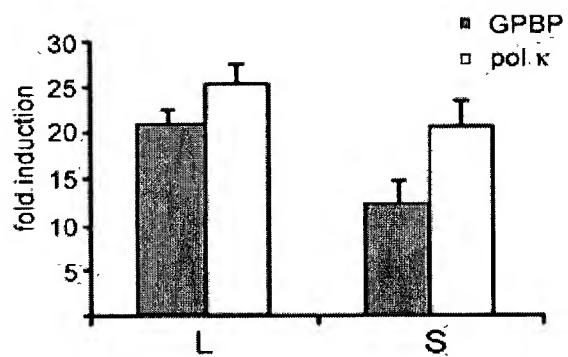
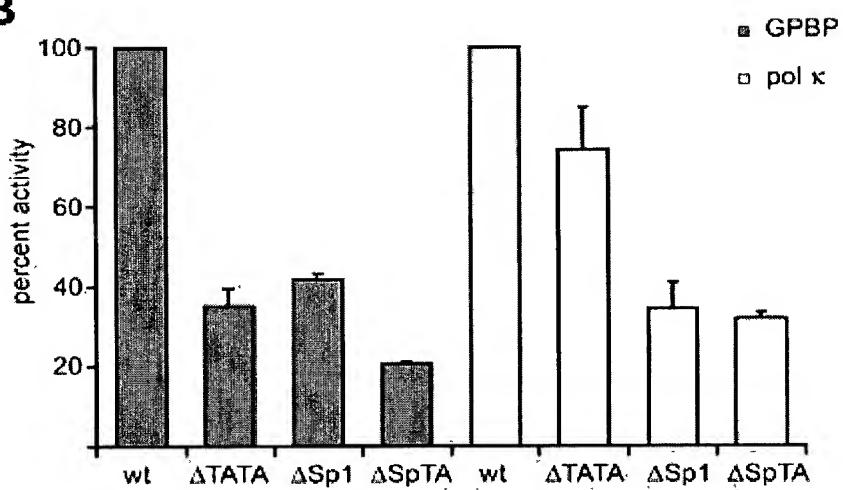
<b>ON-GPPB-18m</b> <pre> GGCATGGTTAACGTGGTTCTCAGGAAGATAATTCAACCAAGAGAAAATCCCAGGCTATCATCTCACATTCTGTGTTTACTTTA CCGTACCAATTGACCAAGAGTCATTCTTAAGTAATGGTTCTCTTCTAGGTAAATGTTAGAGTGTAAAGAACAAATGAAATT </pre>	90
<b>XbaI</b> <pre> AACCTTTCTAACGTCAATTATTCTGACAACCTCAAATTACTTCTAACAAAGCAAACCTAGAAATCTAACCTAGTAAATCTAA TTGGAAGATTGAGTAAATAAGAGACTGTGGAGTTAATGAAAGATGTTGATCTTGTAGATTTTACGCTTCACGCCACGA </pre>	180
<b>TGTGAGAAGGTACTAAGGAATTCTCTTAAACGTCAAATGTGAATTCTAACCTCTAACATTCTAAATGAGTAAGACCCCTCAGATTACAGCGGT ACACTCTTCATGATTCTTAAGGAAGAAATTGAGTGTGGAGTTAACCTTAAGATTGAAGATTACTCATTCGGAGGTCTAAATGTCGCCAC</b>	270
<b>CAGACCACCTTCTGGAAACCGCCCTGGCACTAGTAGCTCACAAAACCCCAGCCCCATGGTTGAGGGGAAGGGCCAGATGCTCCGGGCTTGC AGCTGGTGGAAAGCAGGCCCTGGTGGAAACCGTGATCATCGAGTTGGGGTGGGTACCAACTCCGCTTCGGGGTCTAACGAGGGCCCGAAAG</b>	360
<b>Apal</b> <pre> GACAAGCCGCCCTGGAAGCAGGCCCTGGTCACTTCAGGGAAAGCTCTCACGTCTGGGGCCAAAGGCCGAGGGTTGTCATAAAACA CTGTTGGGGGACCTTCTGTCGGGGCAGTAGAAGTCGGCTTTCGAGAGTGCAGACCCGGGGCTTGGGGCTTCCCAAGCAAGTATTGT </pre>	450
<b>HeLa 4.1</b> ← <pre> CACAGGCAAGGATAGAAGCAGGGCCGAGGGCTGGTCAAGCAACTGTCAAAACGAAGGCCAACCCACCGACTGACAAGGCCAACGGGAC GTGTTCCGTTCTATCTTCGCTCCGGCTCCCGACCAAGTGCAGTTGACTGTGGGTGGCTGACTGTCCGGGGTCTCCCTG </pre>	540



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## FIGURE 1b



**FIGURE 2****A****B**



**FIGURE 3**

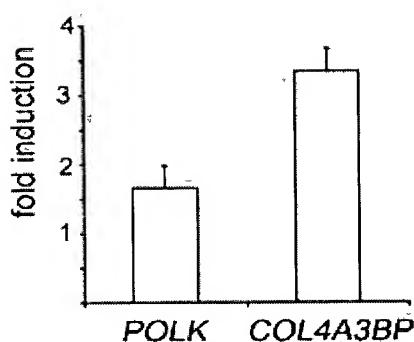
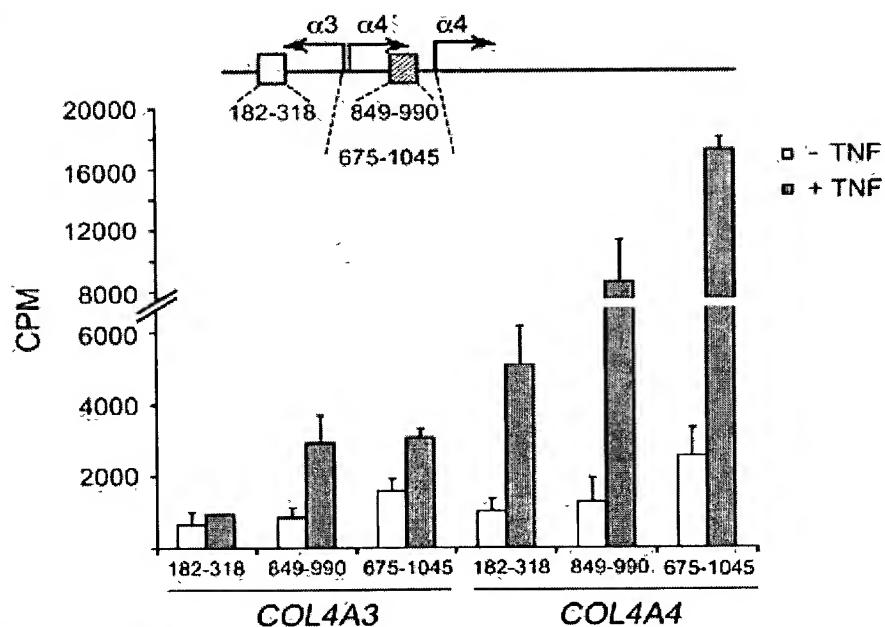
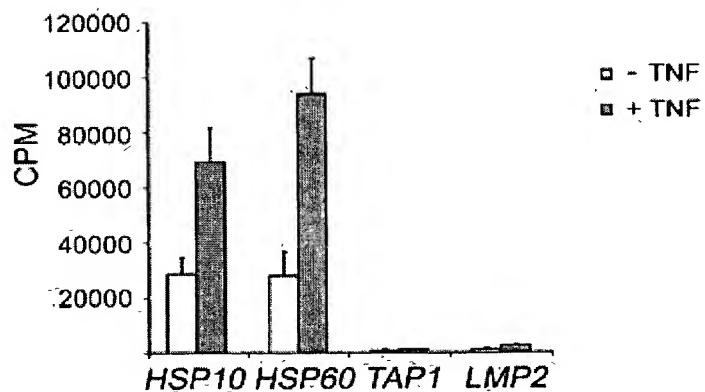
	<i>COL4A3BP</i>		<i>POLK</i>		Alignment map*
<i>COL4A1-A2</i> $(\alpha_1\alpha_2)$ GenBank no. M36963	Region aligned 469-608 $Q=620; E(Q)=591.4 \pm 17.1$ $z=1.6725, P=0.00472$	Region aligned 583-722 $Q=580; E(Q)=571 \pm 19$ $z=0.4737, P=0.3179$			
<i>COL4A3-A4</i> $(\alpha_3\alpha_4)$ GenBank no. AF218541	Region aligned 849-990 $Q=674; E(Q)=568.7 \pm 17.5$ $z=6.0171, P<0.0001$	Region aligned 182-318 $Q=641; E(Q)=557.5 \pm 18.4$ $z=4.5380, P<0.0001$			
<i>COL4A5-A6</i> $(\alpha_5\alpha_6)$ GenBank no. D28116	Region aligned 1714-1853 $Q=570; E(Q)=524.2 \pm 18.4$ $z=2.4891, P=0.0064$	Region aligned 440-579 $Q=570; E(Q)=527.4 \pm 17.3$ $z=2.4624, P=0.0069$			

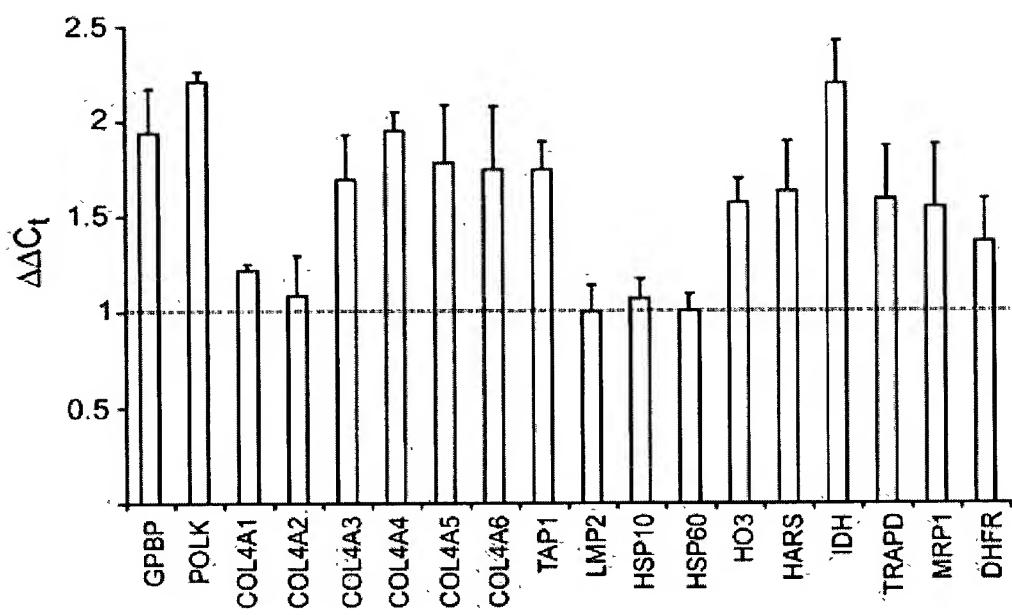


**FIGURE 4**

	<i>COL4A3BP</i>	<i>POLK</i>	Alignment map*
<i>LMP2-TAPI</i>	Region aligned 24579-24718 $Q=61.0; E(Q)=549.9\pm 16.9$ GenBank no. X66401 $z=3.5562, P=\mathbf{0.0002}$	Region aligned 27355-27494 $Q=620; E(Q)=582.8\pm 18.6$ $z=2, P=0.0228$	
<i>MRP1-DHFR</i>	Region aligned 849-991 $Q=581; E(Q)=557.7\pm 20.8$ GenBank no. K01612 $z=1.1202, P=0.1313$	Region aligned 704-843 $Q=640; E(Q)=553.4\pm 18.1$ $z=4.7845, P<0.0001$	
<i>GPAT-AIRC</i>	Region aligned 632-769 $Q=554; E(Q)=573.4\pm 20.4$ GenBank no. U00239 $z=-0.9510, P=0.8292$	Region aligned 561-705 $Q=565; E(Q)=549.4\pm 18.4$ $z=0.8478, P=0.1983$	
<i>HO3-HRS</i>	Region aligned 313-452 $Q=600; E(Q)=531\pm 17.5$ GenBank no. M96646 $z=3.9429, P<\mathbf{0.0001}$	Region aligned 214-353 $Q=560; E(Q)=557.1\pm 16.2$ $z=0.1790, P=0.4290$	
<i>HSP10-HSP60</i>	Region aligned 3451-3590 $Q=600; E(Q)=546.7\pm 16.7$ GenBank no. AJ250915 $z=3.1916, P=\mathbf{0.0007}$	Region aligned 3684-3821 $Q=594; E(Q)=542.6\pm 17.1$ $z=3.0058, P=\mathbf{0.0013}$	
<i>IDHG-TRAPD</i>	Region aligned 16283-16422 $Q=622; E(Q)=594.8\pm 16.5$ GenBank no. Z68129 $z=2.7394, P=0.0031$	Region aligned 14190-14329 $Q=610; E(Q)=601.9\pm 15.5$ $z=0.5226, P=0.3006$	

FIGURE 5

**A****B****C**

**FIGURE 6**

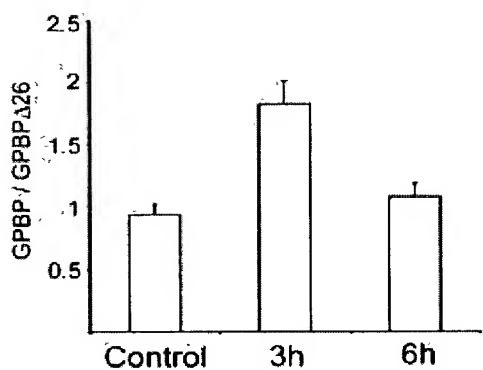
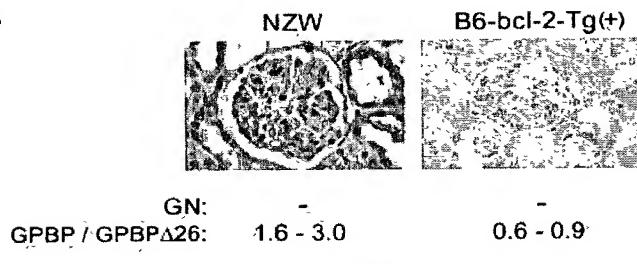
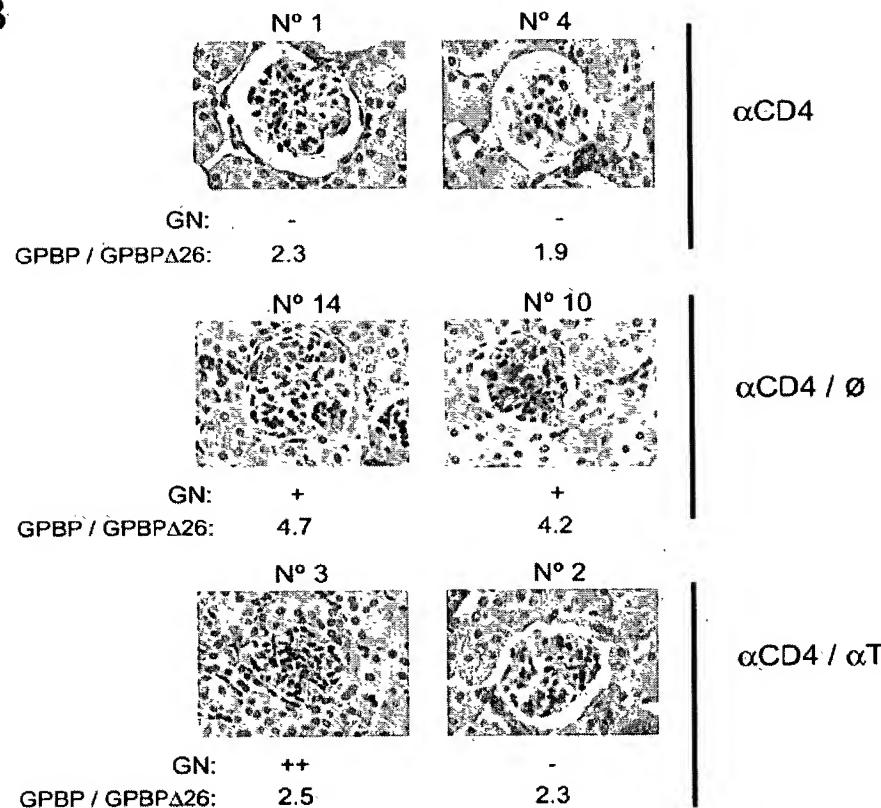
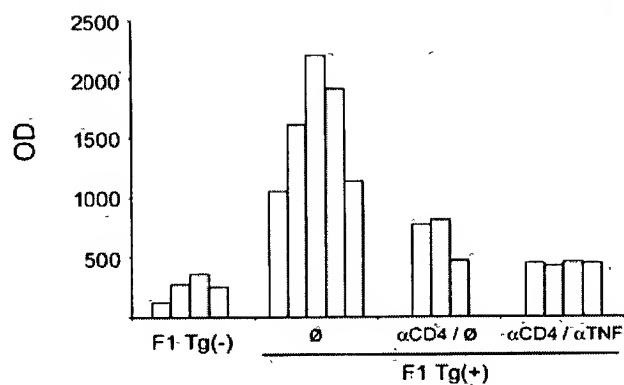
**FIGURE 7**

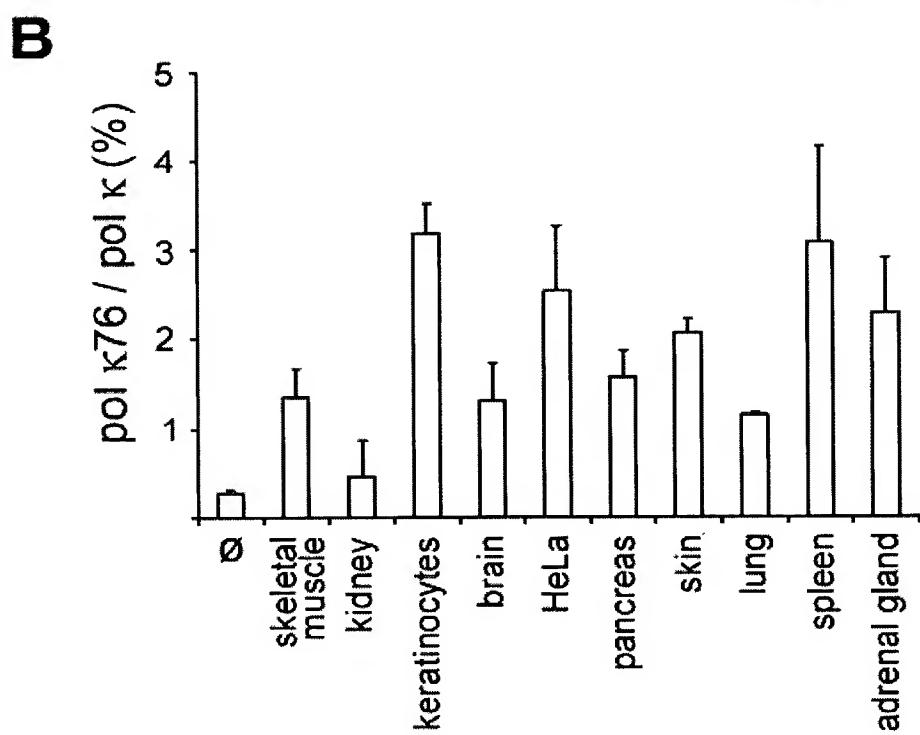
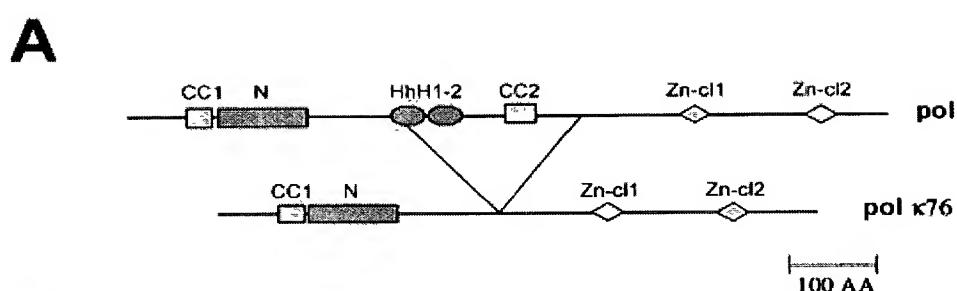


FIGURE 8

**A****B****C**



**FIGURE 9**



**FIGURE 10**